

RAW SEQUENCE LISTING

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Application Serial Number: 09/422,999B
Source: IFW/6
Date Processed by STIC: 6/14/05

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IFW16

RAW SEQUENCE LISTING DATE: 06/14/2005
PATENT APPLICATION: US/09/422,999B TIME: 13:29:06

Input Set : A:\MIT-103.ST25.txt
Output Set: N:\CRF4\06132005\I422999B.raw

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3 <110> APPLICANT: Kawasaki, Hiroaki
4           Graybiel, Ann
5           Housman, David
7 <120> TITLE OF INVENTION: Genes Integrating Signal Transduction Pathways
9 <130> FILE REFERENCE: MIT-103
11 <140> CURRENT APPLICATION NUMBER: US 09/422,999B
12 <141> CURRENT FILING DATE: 1999-10-22
14 <150> PRIOR APPLICATION NUMBER: US 60/105,507
15 <151> PRIOR FILING DATE: 1998-10-23
17 <150> PRIOR APPLICATION NUMBER: US 60/108,685
18 <151> PRIOR FILING DATE: 1998-11-16
20 <160> NUMBER OF SEQ ID NOS: 67
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2250
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (166)..(1989)
34 <400> SEQUENCE: 1
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37 cgggttgca ttctgaagta aaggacttgg gacaggggta cgaatcgagc actgtgggag      120
39 gctctgagag tgtaacttgg gtctagccca ctggcacccg cagcc atg gcg agc act      177
40                               Met Ala Ser Thr
41                               1
43 ctg gac ctg gac aag ggt tgc acc gtc gag gag ctg ctc cgt ggc tgt      225
44 Leu Asp Leu Asp Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys
45 5          10          15          20
47 atc gaa gcc ttt gat gac tct gga aag gtc cga gat cca cag cta gtg      273
48 Ile Glu Ala Phe Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val
49          25          30          35
51 cgc atg ttt ctc atg atg cac ccc tgg tac ata cct tcc tct cag ctg      321
52 Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu
53          40          45          50
55 gct tcg aaa ctg ctc cac ttc tat cag caa tcc cgg aag gac aac tcc      369
56 Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg Lys Asp Asn Ser
57          55          60          65
59 aat tcc cta cag gtc aaa acc tgt cac ctg gtc agg tac tgg gtc tca      417
60 Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg Tyr Trp Val Ser
61          70          75          80
63 gcc ttc cca gca gag ttc gac ttg aac cca gag ctg gct gaa ccg atc      465
64 Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Pro Ile

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65	85	90	95	100	
67	aag gag ctg aag gct ctg tta gac caa gaa gga aac cgc agg cac agc				513
68	Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser				
69	105	110	115		
71	agc ctc atc gac atc gag agt gtc ccc acc tac aag tgg aag cgg cag				561
72	Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln				
73	120	125	130		
75	gtg acc cag cggtt aac cct gtg gaa cag aaa aag cgc aag atg tcc ctg				609
76	Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg Lys Met Ser Leu				
77	135	140	145		
79	ttt ttt gat cac ttg gag cct atg gaa ctg gca gaa cat ctc acc tac				657
80	Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr				
81	150	155	160		
83	ttt gag tat cgg tcc ttc tgc aag atc ctg ttc cag gac tat cac agc				705
84	Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser				
85	165	170	175	180	
87	ttt gtg act cat ggc tgc act gta gac aat ccg gtc ctg gag cga ttc				753
88	Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe				
89	185	190	195		
91	atc tcc ctc ttc aac agt gtc tct cag tgg gtc caa ctc atg atc ctc				801
92	Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu				
93	200	205	210		
95	agc aag ccc aca gcc acg cag cggtt gcg ctg gtc atc aca cat ttc gtg				849
96	Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile Thr His Phe Val				
97	215	220	225		
99	cat gtg gca gag aag ctg ctg cag ctg cag aac ttc aac acg ttg atg				897
100	His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met				
101	230	235	240		
103	gcc gtc gtg gga ggc ctg agc cac agc tcc atc tca cgc ctc aag gag				945
104	Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu				
105	245	250	255	260	
107	acc cac agc cat gtc agc cct gac acc atc aag ctc tgg gaa ggt ctg				993
108	Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu Trp Glu Gly Leu				
109	265	270	275		
111	aca gaa cta gtg aca gct act ggc aac tac agc aac tac cgg cga agg				1041
112	Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn Tyr Arg Arg Arg				
113	280	285	290		
115	ctg gcg gcc tgc gtg ggc ttc cgc ttt cct atc ctg ggt gtg cac ctc				1089
116	Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu				
117	295	300	305		
119	aag gat cta gtg gct ctg cag ctg gct ctg cct gac tgg ctg gac cca				1137
120	Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp Trp Leu Asp Pro				
121	310	315	320		
123	ggt cggtt acc cgg ctc aat gga gcc aag atg agg cag ctt ttc agc att				1185
124	Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln Leu Phe Ser Ile				
125	325	330	335	340	
127	ctg gag gag ttg gct atg gtg acc agt ctt cga cca cca gtg caa gcc				1233
128	Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro Pro Val Gln Ala				
129	345	350	355		

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131 aac ccc gac ctg ctg agt ctg ctc acg gtg tcc ctg gac cag tat cag	1281
132 Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu Asp Gln Tyr Gln	
133 360 365 370	
135 acg gag gat gag ctg tat cag ctc tct ctg cag cga gag cca cgt tcc	1329
136 Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg Glu Pro Arg Ser	
137 375 380 385	
139 aag tca tcg ccc acc agc ccc acc agc tgc acc ccc cct ccc cgg ccc	1377
140 Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro Pro Pro Arg Pro	
141 390 395 400	
143 cct gtg ctg gaa gag tgg acc tca gtt gcc aag cct aag ctg gac caa	1425
144 Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro Lys Leu Asp Gln	
145 405 410 415 420	
147 gcc ttg gtg gcc gag cac att gag aag atg gtg gag tct gtg ttc cgg	1473
148 Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu Ser Val Phe Arg	
149 425 430 435	
151 aac ttt gac gtt gat ggg gac ggt cac atc tcc cag gag gag ttc cag	1521
152 Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln Glu Glu Phe Gln	
153 440 445 450	
155 atc atc cgg ggc aac ttc cct tat ctc agc gcc ttt ggg gac ttg gac	1569
156 Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe Gly Asp Leu Asp	
157 455 460 465	
159 cag aac cag gat ggc tgc atc agc cgg gag gag atg att tcc tac ttc	1617
160 Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met Ile Ser Tyr Phe	
161 470 475 480	
163 ctg cgc tcc agc tcc gtg ctg gga ggc cgc atg ggc ttc gta cac aac	1665
164 Leu Arg Ser Ser Val Leu Gly Gly Arg Met Gly Phe Val His Asn	
165 485 490 495 500	
167 ttc cag gag agt aac tcg cta agg ccg gtc gcc tgc cga cac tgc aaa	1713
168 Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys Arg His Cys Lys	
169 505 510 515	
171 gct ctg atc ctg ggc atc tac aag cag ggc ctc aaa tgt aga gct tgt	1761
172 Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys Cys Arg Ala Cys	
173 520 525 530	
175 ggt gtg aac tgc cac aag cag tgc aaa gac cga ctg tca gtg gaa tgt	1809
176 Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu Ser Val Glu Cys	
177 535 540 545	
179 cgc cgc cgc gcc cag agt gtg agc ctg gag ggc tct gca ccc tct ccc	1857
180 Arg Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser Ala Pro Ser Pro	
181 550 555 560	
183 tca ccc aca cat acc cac cat cgg gcc ttc agc ttc tcc ctg cct cgc	1905
184 Ser Pro Thr His Thr His Arg Ala Phe Ser Phe Ser Leu Pro Arg	
185 565 570 575 580	
187 cca ggc agg cgc agc tct cgg cct cca gag atc cgt gaa gag gag gtg	1953
188 Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg Glu Glu Glu Val	
189 585 590 595	
191 cag act gtg gaa gat ggt gtg ttc gac atc cac tta taagacgctg	1999
192 Gln Thr Val Glu Asp Gly Val Phe Asp Ile His Leu	
193 600 605	
195 tgactatcaa ggactcattc ctgccttgaa gaaaaagactt ggagcagagc agggagccag	2059

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197 ggattctggg gcaggagggtt	ggggctgaag gtgggggaag	ttgaaggtag catgcactga	2119
199 aaaaaaggcc agggctggtg	tccctaaggt tgtacagact	tctgtgaata tttgtatTTT	2179
201 ccagatggaa taaaaaggcc	cgaataatTA acctcgaaaa	aaaaaaaaaaa aaaaaaaaaaa	2239
203 aaaaaaaaaa a			2250
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208 <212> TYPE: PRT			
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221 Pro Gln Leu Val Arg Met Phe Leu Met Met His Pro Trp Tyr Ile Pro			
222 35 40 45			
225 Ser Ser Gln Leu Ala Ser Lys Leu Leu His Phe Tyr Gln Gln Ser Arg			
226 50 55 60			
229 Lys Asp Asn Ser Asn Ser Leu Gln Val Lys Thr Cys His Leu Val Arg			
230 65 70 75 80			
233 Tyr Trp Val Ser Ala Phe Pro Ala Glu Phe Asp Leu Asn Pro Glu Leu			
234 85 90 95			
237 Ala Glu Pro Ile Lys Glu Leu Lys Ala Leu Leu Asp Gln Glu Gly Asn			
238 100 105 110			
241 Arg Arg His Ser Ser Leu Ile Asp Ile Glu Ser Val Pro Thr Tyr Lys			
242 115 120 125			
245 Trp Lys Arg Gln Val Thr Gln Arg Asn Pro Val Glu Gln Lys Lys Arg			
246 130 135 140			
249 Lys Met Ser Leu Leu Phe Asp His Leu Glu Pro Met Glu Leu Ala Glu			
250 145 150 155 160			
253 His Leu Thr Tyr Leu Glu Tyr Arg Ser Phe Cys Lys Ile Leu Phe Gln			
254 165 170 175			
257 Asp Tyr His Ser Phe Val Thr His Gly Cys Thr Val Asp Asn Pro Val			
258 180 185 190			
261 Leu Glu Arg Phe Ile Ser Leu Phe Asn Ser Val Ser Gln Trp Val Gln			
262 195 200 205			
265 Leu Met Ile Leu Ser Lys Pro Thr Ala Thr Gln Arg Ala Leu Val Ile			
266 210 215 220			
269 Thr His Phe Val His Val Ala Glu Lys Leu Leu Gln Leu Gln Asn Phe			
270 225 230 235 240			
273 Asn Thr Leu Met Ala Val Val Gly Gly Leu Ser His Ser Ser Ile Ser			
274 245 250 255			
277 Arg Leu Lys Glu Thr His Ser His Val Ser Pro Asp Thr Ile Lys Leu			
278 260 265 270			
281 Trp Glu Gly Leu Thr Glu Leu Val Thr Ala Thr Gly Asn Tyr Ser Asn			
282 275 280 285			
285 Tyr Arg Arg Arg Leu Ala Ala Cys Val Gly Phe Arg Phe Pro Ile Leu			
286 290 295 300			
289 Gly Val His Leu Lys Asp Leu Val Ala Leu Gln Leu Ala Leu Pro Asp			
290 305 310 315 320			

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293 Trp Leu Asp Pro Gly Arg Thr Arg Leu Asn Gly Ala Lys Met Arg Gln
294 325 330 335
297 Leu Phe Ser Ile Leu Glu Glu Leu Ala Met Val Thr Ser Leu Arg Pro
298 340 345 350
301 Pro Val Gln Ala Asn Pro Asp Leu Leu Ser Leu Leu Thr Val Ser Leu
302 355 360 365
305 Asp Gln Tyr Gln Thr Glu Asp Glu Leu Tyr Gln Leu Ser Leu Gln Arg
306 370 375 380
309 Glu Pro Arg Ser Lys Ser Ser Pro Thr Ser Pro Thr Ser Cys Thr Pro
310 385 390 395 400
313 Pro Pro Arg Pro Pro Val Leu Glu Glu Trp Thr Ser Val Ala Lys Pro
314 405 410 415
317 Lys Leu Asp Gln Ala Leu Val Ala Glu His Ile Glu Lys Met Val Glu
318 420 425 430
321 Ser Val Phe Arg Asn Phe Asp Val Asp Gly Asp Gly His Ile Ser Gln
322 435 440 445
325 Glu Glu Phe Gln Ile Ile Arg Gly Asn Phe Pro Tyr Leu Ser Ala Phe
326 450 455 460
329 Gly Asp Leu Asp Gln Asn Gln Asp Gly Cys Ile Ser Arg Glu Glu Met
330 465 470 475 480
333 Ile Ser Tyr Phe Leu Arg Ser Ser Ser Val Leu Gly Gly Arg Met Gly
334 485 490 495
337 Phe Val His Asn Phe Gln Glu Ser Asn Ser Leu Arg Pro Val Ala Cys
338 500 505 510
341 Arg His Cys Lys Ala Leu Ile Leu Gly Ile Tyr Lys Gln Gly Leu Lys
342 515 520 525
345 Cys Arg Ala Cys Gly Val Asn Cys His Lys Gln Cys Lys Asp Arg Leu
346 530 535 540
349 Ser Val Glu Cys Arg Arg Ala Gln Ser Val Ser Leu Glu Gly Ser
350 545 550 555 560
353 Ala Pro Ser Pro Ser Pro Thr His Thr His His Arg Ala Phe Ser Phe
354 565 570 575
357 Ser Leu Pro Arg Pro Gly Arg Arg Ser Ser Arg Pro Pro Glu Ile Arg
358 580 585 590
361 Glu Glu Glu Val Gln Thr Val Glu Asp Gly Val Phe Asp Ile His Leu
362 595 600 605
365 <210> SEQ ID NO: 3
366 <211> LENGTH: 2236
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
371 <220> FEATURE:
372 <221> NAME/KEY: CDS
373 <222> LOCATION: (161)..(1987)
375 <400> SEQUENCE: 3
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380 ggagcgcagc ctgggccag cccacccgc gccggcggcc atg gca ggc acc ctg 175
381 Met Ala Gly Thr Leu
382 1 5

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/422,999B

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